

AC011175/c
DEFINITION Homo sapiens clone RP11-11014, WAKING DRAFT SEQUENCE, 17 unordered pieces.
VERSION AC011175.5, 11968012
KEYWORDS HTG; HTGS_PIASSETI; HTGS_DRAFT;
organism human.
REFERENCE Eukaryotic Genomes: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo, 1 (bases 1 to 17008)
AUTHORS Birren, B., Clinton, L., Nusbaum, C. and Landier, E.
TITLE Human Sapiens, clone RP11-11013
JOURNAL Unpublished
COMMENT 2 (bases 1 to 17708)
BIRREN, B., CLINTON, L., NUSBAUM, C., LANDIER, E., ALLEN, N., ANDERSON, M., BALCH, J., BEHRE, R., BOEHRINGER, M., DEGENS, P., DE LA PAZ, R., HALL, R., HANSEN, A., CASTRO, A., COLANGELO, M., COLLINS, S., COLLYMORE, A., COOPER, B., FORD, G., FRANK, K., GREEN, M., HARLAND, R., HAYASHI, M., FORRELL, P., FLEISHMAN, J., FORTES, C., FUKU, R., GADE, D., GALAGANI, C., GARDYNSKI, S., GRANT, G., HAGOS, B., HEITOLD, A., HORTON, J., HOWLAND, J., JOHNSON, R., JONES, E., KAMM, L., KARLIS, A., KILIN, J., LEDGER, J., LI, X., LI, Y., LI, Z., MACFARLANE, I., MA, T., MCKERNAN, E., MEYER, A., MCKERNAN, K., MCLENNAN, J., MELDRUM, J., MORROW, J., NEWTON, J., NORMAN, C., O'CONNOR, T., O'DONELL, P., PETROVSKI, K., PILLAI, V., PILLOW, R., REY, A., SAEED, R., SECRET, P., STENOPELIDOU, N., STEPHENSON, N., SUBRAMANIAM, A., THAMES, J., TESTAVERO, S., TORRES, A., VOSSILLO, R., WANG, A., WESTERMARK, W., XYMYDIOU, Y., YO-WUI, J., ZIMMER, A. and ZODDY, M.
DIRECT SUBMISSION
Submitted (11 Oct 1999) Whitehead Institute/MIT Center for Genome Research, 120 Charles Street, Cambridge, MA 02141, USA
or doi: 10.1101/this sequence version replaced at 1734188.
All repeats were identified using RepeatMasker
Smith, A.F.A. & Green, P. (1996-1997)
<http://www.sanger.ac.uk/ftp/b1p/chr11/11013>
Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center of origin: WBFR
Web site: <http://www.gen.wi.mit.edu>
Comments: Sequence submissions genome.wi.mit.edu
Project Information
Center project name: 115.13
Center clone name: 115.13
Summary Statistics
Sequencing vector: Mix: M7745, 100% of reads
Chemistry: dye termination big dye, 100% of reads
Assembly Program: Phrap: version 0.960731
Consensus quality: 167140 bases at least Q40
Consensus quality: 172778 bases at least Q40
Consensus quality: 174418 bases at least Q20
Insert size: 177000; average: 1p
Insert size: 175408; sum of contigs
Quality covarater: 4.1 in Q20 bases; sum of contigs
Quality covarater: 4.2 in Q20 bases; sum of contigs

* NOTE: This is a working draft sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be provisioned.

* 1175: contig of 1175 bp in length
* 176: 1275; gap of 1p
* 127: 2804; contig of 1529 bp in length
* 280: 2704; gap of 194 bp
* 290: 4416; contig of 1512 bp in length
* 441: 4515; gap of 100 bp
* 4517: 7097; contig of 2581 bp in length
* 7099: 7197; gap of 100 bp

[illegible]

